RAW SEQUENCE LISTING   DATE: 12/28/2001
PATENT APPLICATION: US/09/963,679   TIME: 16:12:00

Input Set : A:\032301.232.seq.ST25.txt
Output Set: N:\CRF3\12282001\I963679.raw

ENTERED

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   3 <110> APPLICANT: Farwick, Mike, et al.
   5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dep67 GENE
   7 <130> FILE REFERENCE: 032301 WD 232
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/963,679
C--> 9 <141> CURRENT FILING DATE: 2001-09-27
   9 <160> NUMBER OF SEQ ID NOS: 4
  11 <170> SOFTWARE: PatentIn version 3.1
  13 <210> SEQ ID NO: 1
  14 <211> LENGTH: 1786
  15 <212> TYPE: DNA
  16 <213> ORGANISM: Corynebacterium glutamicum
  18 <220> FEATURE:
  19 <221> NAME/KEY: CDS
  20 <222> LOCATION: (259)..(1560)
  21 <223> OTHER INFORMATION:
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  25 cggcgttttc gagcgggtg tctagcgcaa cgagtgcgga accgcgttgt tgggcctggc    60
  27 tggcgagcat gtgttttgcc acgtcgacgg cattgcgctc ggacttaaaa ttcaacgccg   120
  29 cagatggtgc aagcagctgt gaaatgaggc gtaggcgcg gacgcgttcc agagaaagtg   180
  31 caggcataac ccctaaaata ccctgatctt ccccgtgtc ctgccccgt gtccacccct    240
  33 gcgtacataa taggacgc atg gga aaa cat gag gtt gct cag cag acg gtt    291
  34                     Met Gly Lys His Glu Val Ala Gln Gln Thr Val
  35                       1           5                   10
  37 ccg ggt cct tcg ccg gaa atg gaa gcg cag cgg cgt aaa gag ttg cgc    339
  38 Pro Gly Pro Ser Pro Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg
  39              15              20              25
  41 aag cac aag gcc att gcc act ggc ctg ttg att ttt gct gcc gct gta    387
  42 Lys His Lys Ala Ile Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val
  43          30              35              40
  45 tat ttt ctt tgc cgt ttc gtg gag acc cgt ccg ggt gaa act gca gcg    435
  46 Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala
  47      45              50              55
  49 tgg gta ggt ttt gtg cgc gct gcg gca gag gcc gga atg att ggc ggg    483
  50 Trp Val Gly Phe Val Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly
  51 60              65              70                  75
  53 ttg gcc gac tgg ttc gcg gtc acc gcg ctg ttc cgt cat cca ttg tgg    531
  54 Leu Ala Asp Trp Phe Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp
  55              80              85              90
  57 ctg cct att ccg cac act gcg att atc ccg cgc aag aaa gac cag tta    579
  58 Leu Pro Ile Pro His Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu
  59              95              100             105
  61 ggt gag gcc tta agc ggg ttt gtg ggg gat aac ttc cta aat gcc cag    627
  62 Gly Glu Ala Leu Ser Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln
  63          110             115             120
  65 ctc att acg gaa aaa gtc tct cag gcg cgg atc cca gag cgc gcc ggg    675
  66 Leu Ile Thr Glu Lys Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly
  67      125             130             135
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69  gag tgg ctc gcc cag ccg gaa aac ggg gag aaa gtt tcg cgc gaa gtc   723
70  Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val
71  140             145             150             155
73  ggc aaa ttg acc gct aat att gtg cgc gca atc gat ccg tca gat gct   771
74  Gly Lys Leu Thr Ala Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala
75              160             165             170
77  gaa gcg gtg att aaa tct gcg gtg atc gac aag ctt gcg gaa ccc acc   819
78  Glu Ala Val Ile Lys Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr
79          175             180             185
81  tgg ggc cca cca gct ggg cgg ttg ctg gaa caa ctc ctc gcc gaa gca   867
82  Trp Gly Pro Pro Ala Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala
83          190             195             200
85  aag ccg aac cag ttg tcc agg aac tcg cgc agt ggc tgc aca aaa agg   915
86  Lys Pro Asn Gln Leu Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg
87      205             210             215
89  cgt tgg gct ccc gag ccg ctg att gat cgc ctg ctc aac gag cgc cgc   963
90  Arg Trp Ala Pro Glu Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg
91  220             225             230             235
93  ccg att tgg gcg ccg aaa ttc act gcg cag ctg gtc agc ggc aaa gtc   1011
94  Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val
95              240             245             250
97  tat gac gag gtc ata aaa ttc act gaa gcc gtc gct gcc gat cct aac   1059
98  Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn
99          255             260             265
101 cac gag gcc cgc aaa tcg ctg cgc cga ttc ctt aat aaa ttg gcg caa   1107
102 His Glu Ala Arg Lys Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln
103     270             275             280
105 gac ctg cag cat gac cca ggc atg att att aaa gtt gaa gaa atc aaa   1155
106 Asp Leu Gln His Asp Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys
107     285             290             295
109 cgc gac atc atg ggc tcc ggc gcc atc gcg caa gcc gcg cca acc atc   1203
110 Arg Asp Ile Met Gly Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile
111 300             305             310             315
113 tgg gcg tca gcc tcc gag tcg ctc att gaa tcc gca gaa gat gag tca   1251
114 Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser
115             320             325             330
117 tca att ctg cgt cgc aaa att gcc gaa gca gct acc agc tgg ggt caa   1299
118 Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln
119             335             340             345
121 aga ttg ctt gtc gac gac tcc ctc cgg cat tca ctc gac acc cgg att   1347
122 Arg Leu Leu Val Asp Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile
123     350             355             360
125 acc ggc gcc gct gct ttc ctc gcc gac aat tac gcc ccc gaa gtc acc   1395
126 Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr
127     365             370             375
129 ggc att atc tcc gaa acc att gaa cga tgg gac gct gaa gaa gct tca   1443
130 Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser
131 380             385             390             395
133 gag aaa atc gaa ctc atg gtg ggc aaa gac ctc caa tac atc cgc ctt   1491
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```
134 Glu Lys Ile Glu Leu Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu
                          400             405             410
135
137 aat ggc aca att gta ggt gca tta gca gga ctg gcc att tac gct att      1539
138 Asn Gly Thr Ile Val Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile
139             415             420             425
141 tcc cat atc ctc ttc gga gct taactaggag taaccatcat gtccgatgca         1590
142 Ser His Ile Leu Phe Gly Ala
143             430
145 aaagacgatt ccatcttgtc caagtggagc aatgcagctt ccgagctcag cggtgccgtc    1650
147 agtggagtag cgaagaagct ccgtgaagaa ctctctgaga aggaaacctt cagcaagctt    1710
149 aaaaccgaag ccagcgaagc cgtcgatcaa gcaaagtccg gctcctacct agatgccggt    1770
151 aaggaattcg cccgcg                                                     1786
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 434
156 <212> TYPE: PRT
157 <213> ORGANISM: Corynebacterium glutamicum
159 <400> SEQUENCE: 2
161 Met Gly Lys His Glu Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro
162 1               5                   10                  15
165 Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile
166             20                  25                  30
169 Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg
170             35                  40                  45
173 Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
174             50                  55                  60
177 Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe
178 65                  70                  75                  80
181 Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Pro Ile Pro His
182             85                  90                  95
185 Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
186             100                 105                 110
189 Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
190             115                 120                 125
193 Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
194             130                 135                 140
197 Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
198 145                 150                 155                 160
201 Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
202             165                 170                 175
205 Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
206             180                 185                 190
209 Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala Lys Pro Asn Gln Leu
210             195                 200                 205
213 Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg Arg Trp Ala Pro Glu
214             210                 215                 220
217 Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
218 225                 230                 235                 240
221 Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
222             245                 250                 255
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```
225 Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
226         260                 265                 270
229 Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
230         275                 280                 285
233 Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
234         290                 295                 300
237 Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser
238 305             310                 315                 320
241 Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg
242             325                 330                 335
245 Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp
246         340                 345                 350
249 Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala
250         355                 360                 365
253 Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
254     370                 375                 380
257 Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu
258 385             390                 395                 400
261 Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
262             405                 410                 415
265 Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe
266         420                 425                 430
269 Gly Ala
273 <210> SEQ ID NO: 3
274 <211> LENGTH: 28
275 <212> TYPE: DNA
276 <213> ORGANISM: Corynebacterium glutamicum
278 <400> SEQUENCE: 3
279 gaggtacctc cacccctgcg tacataat                                    28
282 <210> SEQ ID NO: 4
283 <211> LENGTH: 28
284 <212> TYPE: DNA
285 <213> ORGANISM: Corynebacterium glutamicum
287 <400> SEQUENCE: 4
288 tgtctagact agttaagctc cgaagagg                                    28
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/963,679

DATE: 12/28/2001
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

12/28/01